



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/881,509D

DATE: 09/23/2002

TIME: 10:32:08

Input Set : A:\EP.txt

Output Set: N:\CRF3\09232002\H881509D.raw

**Does Not Comply**  
**Corrected Diskette Needed**

## SEQUENCE LISTING

## 7 (1) GENERAL INFORMATION:

9 (i) APPLICANT: SCHENDEL, Dolores J.  
 11 (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA  
 13 (iii) NUMBER OF SEQUENCES: 54  
 15 (iv) CORRESPONDENCE ADDRESS:  
 16 (A) ADDRESSEE: Arent Fox Kintner Plotkin & Kahn  
 17 (B) STREET: 1050 Connecticut Avenue, Suite 400  
 18 (C) CITY: Washington  
 19 (D) STATE: DC  
 20 (E) COUNTRY: USA  
 21 (F) ZIP: 20036-5339  
 23 (v) COMPUTER READABLE FORM:  
 24 (A) MEDIUM TYPE: Floppy disk  
 25 (B) COMPUTER: IBM PC compatible  
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
 29 (vi) CURRENT APPLICATION DATA:  
 C--> 30 (A) APPLICATION NUMBER: US/08/881,509D  
 C--> 31 (B) FILING DATE: 24-Jun-1997  
 32 (C) CLASSIFICATION:  
 34 (viii) ATTORNEY/AGENT INFORMATION:  
 35 (A) NAME: Kitts, Monica Chin  
 36 (B) REGISTRATION NUMBER: 36,105  
 37 (C) REFERENCE/DOCKET NUMBER: 100564-07015  
 39 (ix) TELECOMMUNICATION INFORMATION:  
 40 (A) TELEPHONE: (202) 857-6000  
 41 (B) TELEFAX: (202) 638-4810

## ERRORED SEQUENCES

1098 (2) INFORMATION FOR SEQ ID NO: 46:  
 1100 (i) SEQUENCE CHARACTERISTICS:  
 1101 (A) LENGTH: 13 amino acids  
 1102 (B) TYPE: amino acid  
 1103 (C) STRANDEDNESS: not relevant  
 W--> 1104 (D) TOPOLOGY: not relevant  
 1106 (ii) MOLECULE TYPE: peptide  
 1108 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
 1110 Tyr Cys Leu Val Gly Gly Ser Ala Arg Gln Leu Thr Phe  
 E--> 1111 1 5 10  
 1114 (2) INFORMATION FOR SEQ ID NO: 47:

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```
1116      (i) SEQUENCE CHARACTERISTICS:
1117          (A) LENGTH: 14 amino acids
1118          (B) TYPE: amino acid
1119          (C) STRANDEDNESS: not relevant
W--> 1120          (D) TOPOLOGY: not relevant
1122      (ii) MOLECULE TYPE: peptide
1124      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
1126      Tyr Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe
E--> 1127      1          5          10      15
1130  (2) INFORMATION FOR SEQ ID NO: 48:
1132      (i) SEQUENCE CHARACTERISTICS:
1133          (A) LENGTH: 13 amino acids
1134          (B) TYPE: amino acid
1135          (C) STRANDEDNESS: not relevant
W--> 1136          (D) TOPOLOGY: not relevant
1138      (ii) MOLECULE TYPE: peptide
1140      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
1142      Tyr Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe
E--> 1143      1          5          10      15
1146  (2) INFORMATION FOR SEQ ID NO: 49:
1148      (i) SEQUENCE CHARACTERISTICS:
1149          (A) LENGTH: 13 amino acids
1150          (B) TYPE: amino acid
1151          (C) STRANDEDNESS: not relevant
W--> 1152          (D) TOPOLOGY: not relevant
1154      (ii) MOLECULE TYPE: peptide
1156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
1158      Tyr Cys Leu Val Ser Gly Ser Ala Arg Gln Leu Thr Phe
E--> 1159      1          5          10      15
1162  (2) INFORMATION FOR SEQ ID NO: 50:
1164      (i) SEQUENCE CHARACTERISTICS:
1165          (A) LENGTH: 13 amino acids
1166          (B) TYPE: amino acid
1167          (C) STRANDEDNESS: not relevant
W--> 1168          (D) TOPOLOGY: not relevant
1170      (ii) MOLECULE TYPE: peptide
1172      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:
1174      Tyr Cys Leu Asp Ser Gly Ser Ala Arg Gln Leu Thr Phe
E--> 1175      1          5          10      15
1178  (2) INFORMATION FOR SEQ ID NO: 51:
1180      (i) SEQUENCE CHARACTERISTICS:
1181          (A) LENGTH: 14 amino acids
1182          (B) TYPE: amino acid
1183          (C) STRANDEDNESS: not relevant
W--> 1184          (D) TOPOLOGY: not relevant
1186      (ii) MOLECULE TYPE: peptide
1188      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:
1190      Tyr Cys Leu Val Val Ser Gly Ser Ala Arg Gln Leu Thr Phe
E--> 1191      1          5          10      15
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1194 (2) INFORMATION FOR SEQ ID NO: 52:  
1196 (i) SEQUENCE CHARACTERISTICS:  
1197 (A) LENGTH: 14 amino acids  
1198 (B) TYPE: amino acid  
1199 (C) STRANDEDNESS: not relevant  
W--> 1200 (D) TOPOLOGY: not relevant  
1202 (ii) MOLECULE TYPE: peptide  
1204 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
1206 Tyr Cys Leu Ala Leu Ala Gly Ser Ala Arg Gln Leu Thr Phe  
E--> 1207 1 5 10 15  
1210 (2) INFORMATION FOR SEQ ID NO: 53:  
1212 (i) SEQUENCE CHARACTERISTICS:  
1213 (A) LENGTH: 14 amino acids  
1214 (B) TYPE: amino acid  
1215 (C) STRANDEDNESS: not relevant  
W--> 1216 (D) TOPOLOGY: not relevant  
1218 (ii) MOLECULE TYPE: peptide  
1220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:  
1222 Tyr Cys Leu Ala Pro Ser Gly Ser Ala Arg Gln Leu Thr Phe  
E--> 1223 1 5 10 15  
1226 (2) INFORMATION FOR SEQ ID NO: 54:  
1228 (i) SEQUENCE CHARACTERISTICS:  
1229 (A) LENGTH: 13 amino acids  
1230 (B) TYPE: amino acid  
1231 (C) STRANDEDNESS: not relevant  
W--> 1232 (D) TOPOLOGY: not relevant  
1234 (ii) MOLECULE TYPE: peptide  
1236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
1238 Tyr Cys Leu Val Gly Arg Ser Ala Arg Gln Leu Thr Phe  
E--> 1239 1 5 10 15  
E--> 1244 -22-

## VERIFICATION SUMMARY

PATENT APPLICATION: US/08/881,509D

DATE: 09/23/2002

TIME: 10:32:09

Input Set : A:\EP.txt

Output Set: N:\CRF3\09232002\H881509D.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:436 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:469 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:501 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:533 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:567 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15  
L:600 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:633 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19  
L:682 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23  
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0  
L:700 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24  
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0  
L:718 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25  
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0  
L:736 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26  
L:745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0  
L:754 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27  
L:772 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28  
L:790 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=29  
L:808 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=30  
L:826 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=31  
L:844 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32  
L:862 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=33  
L:880 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=34  
L:898 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=35  
L:916 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=36  
L:934 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=37  
L:952 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=38  
L:970 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=39  
L:988 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=40  
L:1006 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=41  
L:1025 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=42  
L:1044 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=43  
L:1063 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=44  
L:1089 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:1082 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=45  
L:1094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0  
L:1104 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=46  
L:1111 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46  
L:1120 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=47  
L:1127 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47  
L:1136 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=48  
L:1143 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:48  
L:1152 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=49  
L:1159 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:49  
L:1168 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=50

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L:1175 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:50  
L:1184 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=51  
L:1191 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:51  
L:1200 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=52  
L:1207 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:52  
L:1216 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=53  
L:1223 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:53  
L:1232 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=54  
L:1239 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54  
M:332 Repeated in SeqNo=54

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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